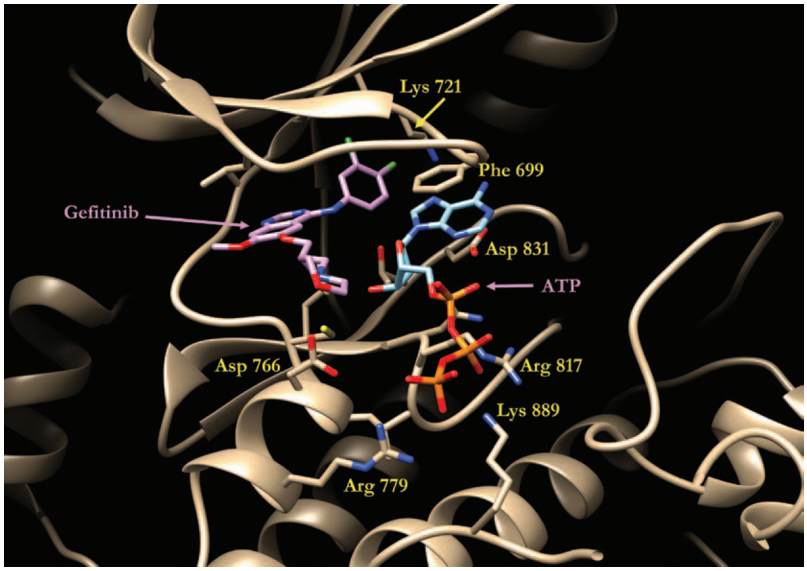

FIGURE 3. Predicted protein structure of the double mutant E746V-L747P. This structural rearrangement allows ATP (orange and blue chemical structure) binding, even in the presence of gefitinib (purple chemical structure), in a favorable position for hydrolysis. Visual analysis of the protein structures based on native EGFR alone, in complex either with tyrosine kinase inhibitor or ATP analogue, mutated EGFR with gefitinib from Protein Data Bank (http://www.rcsb.org/pdb/home/home.do. Accessed February 10, 2015; PDB: 4WRG, 4WKQ, 4HJO, 4G5J, 4I23, 3VJO, 4I22), was carried over using the program COOT and figure was drawn using the program Chimera.

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ACKNOWLEDGEMENTS

The present study was supported by "Fondazione Carige" (2013.0277-12) and the Italian Ministry of Health (GR 2011-12; 02350922; SC). We thank Drs. Cristina Bruzzo and Zita Cavalieri for technical support. We are grateful to the tissue bank Centro di Risorse Biologiche-IST (CRB-IST).

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MicroRNA Assays for Diagnosis Lung Cancer Biopsy

To the Editor:

The recent report on "MicroRNA Assays to Distinguish Squamous Cell Carcinoma from Adenocarcinoma in Lung Cancer Biopsies" is very interesting.[1] Patnaik et al.[1] noted that "histotypic microRNA assays can aid the subtyping of non-small-cell lung cancer biopsies as

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DOI: 10.1097/JTO.0000000000000528

ISSN: 1556-0864/15/1006-0e52

adenocarcinoma (AC) or squamous cell carcinoma (SCC) by standard histopathologic methods." In fact, adding a new diagnostic tool to the classical diagnostic tool might improve the diagnostic ability. Focusing on the use of microRNAassays, there are still left concern and questions on the cost effectiveness, availability, and complexity of the tests. These points have to be further discussed. Focusing on MiR-205 MicroRNA, its diagnostic value for differentiating between AC and SCC is still controversial. Some previous reports showed limitation of its ability to diagnose SCC.[2] Also, the MiR-205 can also increase in the case with severe inflammation and benign tumor.[3] The possibility of false-positive because of noncancerous lesion has to be further studied.

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Reply to "MiR-205 and miR-375 microRNA Assays to Distinguish Squamous Cell Carcinoma From Adenocarcinoma in Lung Cancer Biopsies"

In Response:

We thank Dr. Wiwanitkit for his comments on our study.[1] The microRNA-based assay described in it requires the quantification of only four RNAs (*miR-21*, *miR-205*, and *miR-375*, and *RNU6B*). As already noted by us in the publication, this can be conveniently done in any laboratory with a quantitative polymerase chain reaction machine, with time and material costs similar to those for immunohistochemistry-based diagnosis of non–small-cell lung cancer histology. However, the suitability of the assay for biospecimens with less than 90% tumor content has not been assessed by us. In our study, microdissection of tumor-containing regions of biopsied material was performed for 76% of biopsies to have ≥90% tumor content in the specimens that were used for RNA extraction for the microRNA-based assay.

The studies on the association of *miR-205* with severe inflammation and benign tumor and the lack of a differential expression of this microRNA between normal and tumor tissues, which Dr. Wiwanitkit refers to, concern oral cancer and not cancer of the lung. In case of the latter, a significantly higher expression of *miR-205* in lung squamous cell carcinoma tissue compared with normal lung, or lung tissue with adenocarcinoma or benign diseases has been noted by many[2–5] and in Figure 1 of our article.[1]

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ISSN: 1556-0864/15/1006-0e53

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Reply to "Better Prognostic Models May Result in Improved Patient Selection for Adjuvant Therapies After Complete Resection of Solitary Fibrous Tumors of the Pleura"

In Response:

We would like to thank Dr. Tapias and Dr. Lanuti for their comments on our recent article reporting on a multicenter cohort of 68 patients with solitary fibrous tumors of the pleura (SFTP), who were analyzed for the complete course of the disease in a routine practice setting.[1] We acknowledge that our recurrence rate of 30%

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DOI: 10.1097/JTO.0000000000000557

ISSN: 1556-0864/15/1006-0e53